

SEQUENCE LISTING

SEQ ID NO: 1 is mouse TECK nucleotide sequence.
SEQ ID NO: 2 is mouse TECK amino acid sequence.
SEQ ID NO: 3 is human TECK nucleotide sequence.
SEQ ID NO: 4 is human TECK amino acid sequence.
SEQ ID NO: 5 is human MIP-3 α nucleotide sequence.
SEQ ID NO: 6 is human MIP-3 α amino acid sequence.
SEQ ID NO: 7 is human MIP-3 β nucleotide sequence.
SEQ ID NO: 8 is human MIP-3 β amino acid sequence.
SEQ ID NO: 9 is human DC CR nucleotide sequence.
SEQ ID NO: 10 is human DC CR amino acid sequence.
SEQ ID NO: 11 is human M/DC CR nucleotide sequence.
SEQ ID NO: 12 is human M/DC CR amino acid sequence.
SEQ ID NO: 13 is human CCKR1 amino acid sequence.
SEQ ID NO: 14 is human CCKR2 amino acid sequence.
SEQ ID NO: 15 is human CCKR3 amino acid sequence.
SEQ ID NO: 16 is human CCKR4 amino acid sequence.
SEQ ID NO: 17 is HPRT sense primer.
SEQ ID NO: 18 is HPRT antisense primer.
SEQ ID NO: 19 is FLAG epitope tag sequence.
SEQ ID NO: 20 is TECK sense primer
SEQ ID NO: 21 is TECK antisense primer
SEQ ID NO: 22 is exon 1-specific CRAM primer
SEQ ID NO: 23 is exon 2-specific CRAM primer
SEQ ID NO: 24 is exon 3-specific CRAM primer
SEQ ID NO: 25 is CRAM primer
SEQ ID NO: 26 is CRAM primer

<110> Wang, Wei

Gish, Kurt C.

Schall, Thomas J.

Vicari, Alain P.

Zlotnik, Albert

<120> Methods for using chemokine TECK

<130> DX0589K1D US

<150> US 10/039,659

<151> 2002-01-03

<150> US 08/887,977

<151> 1997-07-03

<150> US 60/021,664

<151> 1996-07-05

<150> US 60/028,329

<151> 1996-10-11

<150> US 60/048,593

<151> 1997-06-04

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<170> PatentIn version 3.1

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<222> (94) .. (525)

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Met Lys Leu Trp Leu Phe Ala	
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tgc ctg gtt gcc tgt ttt gtt ggg gcc tgg atg ccg gtt gtc cat gcc	162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala	
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Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys	
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Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val	
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Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile	
75 80 85	
ttg aca gct agg aaa agg cta gtc cac tgg aag agc gcc tca gac tct	402
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser	
90 95 100	
cag act gaa agg aag aag tca aac cat atg aag tcc aag gtg gag aac	450
Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn	
105 110 115	
ccc aac agt aca agc gtg agg agt gcc acc cta ggt cat ccc agg atg	498
Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met	
120 125 130 135	
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Val Met Met Pro Arg Lys Thr Asn Asn	
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gaagaagaca ttaacaggag agagaggagc gagaggatag tgagtgtgtg agagtgcctg	965
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Gly	Tyr	Gln	His	Arg	Ile	Lys	Trp	Asn	Val	Leu	Arg	His	Ala	Arg	Asn
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Tyr	His	Gln	Gln	Glu	Val	Ser	Gly	Ser	Cys	Asn	Leu	Arg	Ala	Val	Arg
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Val	Lys	Arg	Ala	Ile	Arg	Ile	Leu	Thr	Ala	Arg	Lys	Arg	Leu	Val	His
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Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr Tyr
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cgg atc cag gag gtg agc ggg agc tgc aat ctg cct gct gcg ata ttc 311
Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile Phe
30 35 40

tac ctc ccc aag aga cac agg aag gtg tgt ggg aac ccc aaa agc agg 359
Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser Arg
45 50 55

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Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val Phe
60 65 70

gca aag ctc cac cac aac atg cag acc ttc caa gca ggc cct cat gct 455
 Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His Ala
 75 80 85 90

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 Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe
 95 100 105

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 Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser
 110 115 120

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 Ala Asn Ser Gly Leu
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Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
 30 35 40

Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
 45 50 55

Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
 60 65 70

Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His
 75 80 85

Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys
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 -10 -5 -1 1 5

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 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
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ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc 192
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
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ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act 240
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tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg 288
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
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Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
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Glu	Asp	Cys	Cys	Leu	Ser	Val	Thr	Gln	Lys	Pro	Ile	Pro	Gly	Tyr	Ile		
			30					35					40				
gtg	agg	aac	ttc	cac	tac	ctt	ctc	atc	aag	gat	ggc	tgc	agg	gtg	cct		315
Val	Arg	Asn	Phe	His	Tyr	Leu	Leu	Ile	Lys	Asp	Gly	Cys	Arg	Val	Pro		
		45					50					55					
gct	gta	gtg	ttc	acc	aca	ctg	agg	ggc	cgc	cag	ctc	tgt	gca	ccc	cca		363
Ala	Val	Val	Phe	Thr	Thr	Leu	Arg	Gly	Arg	Gln	Leu	Cys	Ala	Pro	Pro		
	60					65				70							
gac	cag	ccc	tgg	gta	gaa	cgc	atc	atc	cag	aga	ctg	cag	agg	acc	tca		411
Asp	Gln	Pro	Trp	Val	Glu	Arg	Ile	Ile	Gln	Arg	Leu	Gln	Arg	Thr	Ser		
	75				80				85					90			
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Ala	Lys	Met	Lys	Arg	Arg	Ser	Ser										
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Val	Thr	Gln	Lys	Pro	Ile	Pro	Gly	Tyr	Ile	Val	Arg	Asn	Phe	His	Tyr		
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att act cag ttg att ctg aga tgt tac tgt gct cct tgc agg agg tca 96
 Ile Thr Gln Leu Ile Leu Arg Cys Tyr Cys Ala Pro Cys Arg Arg Ser
 20 25 30

ggc agt tct cca ggc tat ttg tac cga att gcc tac tcc ttg atc tgt 144
 Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
 35 40 45

gtt ctt ggc ctc ctg ggg aat att ctg gtg gtg atc acc ttt gct ttt 192
 Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
 50 55 60

tat aag aag gcc agg tct atg aca gac gtc tat ctc ttg aac atg gcc 240
 Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
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att gca gac atc ctc ttt gtt ctt act ctc cca ttc tgg gca gtg agt Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser 85 90 95	288
cat gcc act ggt gcg tgg gtt ttc agc aat gcc acg tgc aag ttg cta His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu 100 105 110	336
aaa ggc atc tat gcc atc aac ttt aac tgc ggg atg ctg ctc ctg act Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr 115 120 125	384
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tac acg ttc att gtc aaa acc ttg gtg caa gct cag aat tct aaa agg Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg 225 230 235 240	720
cac aaa gcc atc cgt gta atc ata gct gtg gtg ctt gtg ttt ctg gct His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala 245 250 255	768
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 325 330 335

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 340 345 350

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Gly Ser Ser Pro Gly Tyr Leu Tyr Arg Ile Ala Tyr Ser Leu Ile Cys
 35 40 45

Val Leu Gly Leu Leu Gly Asn Ile Leu Val Val Ile Thr Phe Ala Phe
 50 55 60

Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
 65 70 75 80

Ile Ala Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Ser
 85 90 95

His Ala Thr Gly Ala Trp Val Phe Ser Asn Ala Thr Cys Lys Leu Leu
 100 105 110

Lys Gly Ile Tyr Ala Ile Asn Phe Asn Cys Gly Met Leu Leu Leu Thr
 115 120 125

Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
 130 135 140

Phe Arg Leu Arg Ser Arg Thr Leu Pro Arg Ser Lys Ile Ile Cys Leu
 145 150 155 160

Val Val Trp Gly Leu Ser Val Ile Ile Ser Ser Ser Thr Phe Val Phe
 165 170 175

Asn Gln Lys Tyr Asn Thr Gln Gly Ser Asp Val Cys Glu Pro Lys Tyr
 180 185 190

Gln Thr Val Ser Glu Pro Ile Arg Trp Lys Leu Leu Met Leu Gly Leu
 195 200 205

Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Met Phe Met Ile Phe Cys
 210 215 220

Tyr Thr Phe Ile Val Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
 225 230 235 240

His Lys Ala Ile Arg Val Ile Ile Ala Val Val Leu Val Phe Leu Ala
 245 250 255

Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Leu
 260 265 270

Gly Lys Met Asn Arg Ser Cys Gln Ser Glu Lys Leu Ile Gly Tyr Thr
 275 280 285

Lys Thr Val Thr Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
 290 295 300

Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Leu Lys
 305 310 315 320

Ile Leu Lys Asp Leu Trp Cys Val Arg Arg Lys Tyr Lys Ser Ser Gly
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Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr Thr Leu Ala
5 10 15

cca gag gat gaa tat gat gtc ctc ata gaa ggt gaa ctg gag agc gat 153
Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu Glu Ser Asp
20 25 30 35

gag gca gag caa tgt gac aag tat gac gcc cag gca ctc tca gcc cag 201
Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu Ser Ala Gln
40 45 50

ctg gtg cca tca ctc tgc tct gct gtg ttt gtg atc ggt gtc ctg gac 249
Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly Val Leu Asp
55 60 65

aat ctc ctg gtt gtg ctt atc ctg gta aaa tat aaa gga ctc aaa cgc 297
Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly Leu Lys Arg
70 75 80

gtg gaa aat atc tat ctt cta aac ttg gca gtt tct aac ttg tgt ttc	345
Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu Cys Phe	
85 90 95	
ttg ctt acc ctg ccc ttc tgg gct cat gct ggg ggc gat ccc atg tgt	393
Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys	
100 105 110 115	
aaa att ctc att gga ctg tac ttc gtg ggc ctg tac agt gag aca ttt	441
Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser Glu Thr Phe	
120 125 130	
ttc aat tgc ctt ctg act gtg caa agg tac cta gtg ttt ttg cac aag	489
Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys	
135 140 145	
ggc aac ttt ttc tca gcc agg agg agg gtg ccc tgt ggc atc att aca	537
Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Ile Thr	
150 155 160	
agt gtc ctg gca tgg gta aca gcc att ctg gcc act ttg cct gaa ttc	585
Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu Pro Glu Phe	
165 170 175	
gtg gtt tat aaa cct cag atg gaa gac cag aaa tac aag tgt gca ttt	633
Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys Cys Ala Phe	
180 185 190 195	
agc aga act ccc ttc ctg cca gct gat gag aca ttc tgg aag cat ttt	681
Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp Lys His Phe	
200 205 210	
ctg act tta aaa atg aac att tcg gtt ctt gtc ctc ccc cta ttt att	729
Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro Leu Phe Ile	
215 220 225	
ttt aca ttt ctc tat gtg caa atg aga aaa aca cta agg ttc agg gag	777
Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe Arg Glu	
230 235 240	
cag agg tat agc ctt ttc aag ctt gtt ttt gcc gta atg gta gtc ttc	825
Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met Val Val Phe	
245 250 255	
ctt ctg atg tgg gcg ccc tac aat att gca ttt ttc ctg tcc act ttc	873
Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe	
260 265 270 275	
aaa gaa cac ttc tcc ctg agt gac tgc aag agc agc tac aat ctg gac	921
Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr Asn Leu Asp	
280 285 290	
aaa agt gtt cac atc act aaa ctc atc gcc acc acc cac tgc tgc atc	969
Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His Cys Cys Ile	
295 300 305	

aac cct ctc ctg tat gcg ttt ctt gat ggg aca ttt agc aaa tac ctc 1017
Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser Lys Tyr Leu
310 315 320

tgc	cgc	tgt	ttc	cat	ctg	cgt	agt	aac	acc	cca	ctt	caa	ccc	agg	ggg	1065
Cys	Arg	Cys	Phe	His	Leu	Arg	Ser	Asn	Thr	Pro	Leu	Gln	Pro	Arg	Gly	
	325					330					335					

cag tct gca caa ggc aca tcg agg gaa gaa cct gac cat tcc acc gaa 1113
Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His Ser Thr Glu
340 345 350 355

gtg taaactagca tccaccaaat gcaagaagaa taaacatgga ttttcatctt 1166
Val

tctgcattat ttcatgtaaa ttttctacac atttgtatac aaaatcggat acaggaagaa 1226

aagggagagg tgagctaaca ttgctaagc actgaatttg tctcaggcac cgtgcaaggc 1286

tctttacaaa cgtgagctcc ttcgcctcct accacttgtc catagtgtgg ataggactag 1346

tctcatttct ctgagaagaa aactaaggcg cggaaatttg tctaagatca cataactagg 1406

aagtggcaga actgattctc cagccctggg agcatttgct cagagcctac gcttgggtcca 1466

gaacatcaaa ctccaaaccc tggggacaaa cgacatgaaa taaatgtatt ttaaaacata 1526

taaaaaaaaaa aaaaaaaaaa a 1547

<210> 12

<211> 356

<212> PRT

<213> Homo sapiens

<400> 12

Met Ile Tyr Thr Arg Phe Leu Lys Gly Ser Leu Lys Met Ala Asn Tyr
1 5 10 15

Thr Leu Ala Pro Glu Asp Glu Tyr Asp Val Leu Ile Glu Gly Glu Leu
20 25 30

Glu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr Asp Ala Gln Ala Leu
35 40 45

Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe Val Ile Gly
50 55 60

Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys Gly
65 70 75 80

Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn
85 90 95

Leu Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp
100 105 110

Pro Met Cys Lys Ile Leu Ile Gly Leu Tyr Phe Val Gly Leu Tyr Ser
115 120 125

Glu Thr Phe Phe Asn Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe
130 135 140

Leu His Lys Gly Asn Phe Phe Ser Ala Arg Arg Arg Val Pro Cys Gly
145 150 155 160

Ile Ile Thr Ser Val Leu Ala Trp Val Thr Ala Ile Leu Ala Thr Leu
165 170 175

Pro Glu Phe Val Val Tyr Lys Pro Gln Met Glu Asp Gln Lys Tyr Lys
180 185 190

Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu Thr Phe Trp
195 200 205

Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu Pro
210 215 220

Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg
225 230 235 240

Phe Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Val Met
245 250 255

Val Val Phe Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu
260 265 270

Ser Thr Phe Lys Glu His Phe Ser Leu Ser Asp Cys Lys Ser Ser Tyr
 275 280 285

Asn Leu Asp Lys Ser Val His Ile Thr Lys Leu Ile Ala Thr Thr His
 290 295 300

Cys Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Asp Gly Thr Phe Ser
 305 310 315 320

Lys Tyr Leu Cys Arg Cys Phe His Leu Arg Ser Asn Thr Pro Leu Gln
 325 330 335

Pro Arg Gly Gln Ser Ala Gln Gly Thr Ser Arg Glu Glu Pro Asp His
 340 345 350

Ser Thr Glu Val
 355

<210> 13

<211> 355

<212> PRT

<213> Homo sapiens

<400> 13

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60

Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
85 90 95

Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Leu Ser Gly Phe
100 105 110

Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Leu
145 150 155 160

Ala Ile Leu Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
165 170 175

Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
180 185 190

Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220

Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Thr Pro Tyr Asn
245 250 255

Leu Thr Ile Leu Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
260 265 270

Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
275 280 285

Ile Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg Gln Leu Phe His Arg Arg Val
 305 310 315 320

Ala Val His Leu Val Lys Trp Leu Pro Phe Leu Ser Val Asp Arg Leu
 325 330 335

Glu Arg Val Ser Ser Thr Ser Pro Ser Thr Gly Glu His Glu Leu Ser
 340 345 350

Ala Gly Phe
 355

<210> 14

<211> 374

<212> PRT

<213> Homo sapiens

<400> 14

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
 1 5 10 15

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 20 25 30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 50 55 60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
 85 90 95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320

Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 325 330 335

Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350

Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
 355 360 365

Gln Asp Lys Glu Gly Ala
 370

<210> 15

<211> 355

<212> PRT

<213> Homo sapiens

<400> 15

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
 1 5 10 15

Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
 20 25 30

Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
 35 40 45

Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
 50 55 60

Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
 85 90 95

His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
 100 105 110

Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125

Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
 130 135 140

Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
 145 150 155 160

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
 165 170 175

Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
 180 185 190

Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
 195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
 210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
 225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
 245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
 260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
 275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
 290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
 305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
 325 330 335

Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
 340 345 350

Ile Val Phe
355

<210> 16

<211> 360

<212> PRT

<213> Homo sapiens

<400> 16

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
 165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
 245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350

Asp His Asp Leu His Asp Ala Leu
 355 360

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT sense primer

<400> 17

gtaatgatca gtcaacgggg gac

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> HPRT antisense primer

<400> 18

ccagcaagct tgcaacctta acca

24

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG epitope tag sequence

<400> 19

Asp Tyr Lys Asp Asp Asp Asp Lys Leu
1 5

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK sense primer

<400> 20

ccttcaggta tctggagagg agatc

25

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> TECK antisense primer

<400> 21

cacgcttgta ctggtgggggt tc

22

<210> 22

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 1-specific CRAM primer

<400> 22

agacgcttca gagatcctct ggaggcc

27

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 2-specific CRAM primer

<400> 23

gaagctgctt cggggggtga gcaaac

26

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> exon 3-specific CRAM primer

<400> 24

caaacacagc agagcagagt gatggcacc

29

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 25

gtgtcctggc atgggtaaca gcc

23

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> CRAM primer

<400> 26

cggtggaatg gtcaggttct tccc

24